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ORIGIN

11

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 361 caatcccacc actgtttgct ggagaatcag tgttccaaat caactttcaa tgggatgaaa
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Oct 4 2004 14:35:49

- L35 ANSWER 13 OF 14 CAPLUS COPYRIGHT 2004 ACS on STN
- AN 1998:97895 CAPLUS
- DN 128:191696

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- TI Progress towards engineering the composition and quantity of plant oils
- AU Ohlrogge, J.; Bao, Xiaoming; Cahoon, E.; Dormann, P.; Eccleston, V.; Roesler, K.; Shintani, D.; Shorrosh, B.
- CS Dept. of Botany and Plant Pathology, Michigan State University, East Lansing, MI, 48824, USA
- SO Oils-Fats-Lipids 1995, Proceedings of the World Congress of the International Society for Fat Research, 21st, The Hague, Oct. 1-6, 1995 (1996), Meeting Date 1995, Volume 1, 75-79 Publisher: P.J. Barnes & Associates, Bridgwater, UK.
 - CODEN: 65QOAT
- DT Conference; General Review
- LA English
- AB A review and discussion with 13 refs. Spurred in part by industrial interest in genetic engineering of plant oils, progress in plant fatty acid and glycerolipid synthesis has been impressive in the past 2-5 yr. Some recent accomplishments in this field include: (1) cloning of many soluble and membrane-bound desaturases including: . **DELTA.4**, $\Delta 6$, $\Delta 9$, $\Delta 12$, and $\omega 3$ desaturases; (2) the first crystallization and x-ray structure of a fatty acid desaturase; (3) cloning of both soluble glycerol-3-phosphate and membrane-bound monoacyl-glycerol-3-phosphate acyl-transferases; (4) cloning of several membrane-bound fatty acid elongases; and (5) major alterations in oil production in transgenic plants. Production of 1 million pounds of high laurate rapeseed oil this year and alteration of saturated and unsatd. fatty acid contents of major oil crops have been achieved. Although there are now many successes in altering the types of fatty acids produced in oilseeds, increases in oil quantity have not yet been reported using mol. genetic approaches. Acetyl-CoA carboxylase (ACCase) is a likely regulatory point which controls the flux of carbon into the fatty acid biosynthetic pathway. However, it is not known if the production of oil in seeds can be controlled by the expression level of this enzyme. To address this issue both cytosolic and plastidial isoenzymes of acetyl-CoA carboxylase have been cloned and characterized. Transgenic plants have

been produced which over-express and under-express ACCase.

RESULT 4 CSLBLOX LOCUS mRNA linear PLN 18-MAR-2001 CSLBLOX 2964 bp DEFINITION C.sativus mRNA for lipoxygenase. ACCESSION X92890 VERSION X92890.1 GI:1296511 KEYWORDS lipoxygenase. Cucumis sativus (cucumber) SOURCE ORGANISM Cucumis sativus Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis. REFERENCE Hohne, M., Nellen, A., Schwennesen, K. and Kindl, H. AUTHORS TITLE Lipid body lipoxygenase characterized by protein fragmentation, cDNA sequence and very early expression of the enzyme during germination of cucumber seeds JOURNAL Eur. J. Biochem. 241 (1), 6-11 (1996) MEDLINE 97054584 PUBMED 8898881 REFERENCE 2 (bases 1 to 2964) AUTHORS Kindl, H. TITLE Direct Submission JOURNAL Submitted (10-NOV-1995) H. Kindl, FB Chemie, Universitat Marburg, Hans-Meerwein-Strasse, D- Marburg, FRG **FEATURES** Location/Qualifiers 1. .2964 source /organism="Cucumis sativus" /mol type="mRNA" /db xref="taxon:3659" /clone="pCSLBLOX221" /tissue_type="cotyledones" /clone lib="pSPORT 1" CDS 48. .2684 /EC number="1.13.11.12" /codon start=1 /product="lipoxygenase" /protein id="CAA63483.1" /db xref="GI:1296512" /db xref="SPTREMBL:Q42710" /translation="MFGIGKNIIEGALNTTGDLAGSVINAGGNILDRVSSLGGNKIKG KVILMRSNVLDFTEFHSNLLDNFTELLGGGVSFQLISATHTSNDSRGKVGNKAYLERW LTSIPPLFAGESVFQINFQWDENFGFPGAFFIKNGHTSEFFLKSLTLDDVPGYGRVHF DCNSWVYPSGRYKKDRIFFANHVYLPSQTPNPLRKYREEELWNLRGDGTGERKEWDRI YDYDVYNDIADPDVGDHRPILGGTTEYPYPRRGRTGRPRSRRDHNYESRLSPIMSLDI YVPKDENFGHLKMSDFLGYTLKALSISIKPGLQSIFDVTPNEFDNFKEVDNLFERGFP IPFNAFKTLTEDLTPPLFKALVRNDGEKFLKFPTPEVVKDNKIGWSTDEEFAREMLAG PNPLLIRRLEAFPPTSKLDPNVYGNQNSTITEEHIKHGLDGLTVDEAMKQNRLYIVDF HDALMPYLTRMNATSTKTYATRTLLLLKDDGTLKPLVIELALPHPQGDQLGAISKLYF PAENGVQKSIWQLAKAYVTVNDVGYHQLISHWLHTHAVLEPFVIATHRQLSVLHPIHK LLVPHYKDTMFINASARQVLINANGLIETTHYPSKYSMELSSILYKDWTFPDQALPNN LMKRGLAVEDSSAPHGLRLLINDYPFAVDGLDIWSAIKTWVQDYCCLYYKDDNAVQND FELQSWWNELREKGHADKKHEPWWPKMQTLSELIESCTTIIWIASALHAAVNFGQYPY GGYILNRPTTSRRFMPEVGTAEYKELESNPEKAFLRTICSELQALVSISIIEILSKHA

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100.0%; Query Match Score 732; DB 8; Length 2964; 100.0%; Pred. No. 1.6e-155; Best Local Similarity Indels 732; Conservative 0; Mismatches Gaps 0; 1 ATGTTTGGAATTGGGAAGAACATCATTGAAGGGGCCTTGAATACAACTGGAGATCTTGCA 60 Qу ATGTTTGGAATTGGGAAGACATCATTGAAGGGGCCTTGAATACAACTGGAGATCTTGCA 107 Db 61 GGTTCTGTTATCAATGCTGGTGGTAACATTTTAGATAGAGTTTTCCAGTCTTGGAGGAAAC 120 Qy 108 GGTTCTGTTATCAATGCTGGTGGTAACATTTTAGATAGAGTTTCCAGTCTTGGAGGAAAC 167 Db Qy 121 AAAATCAAAGGGAAAGTGATTCTTATGAGAAGCAATGTTTTGGATTTCACTGAATTTCAT 180 Db 168 AAAATCAAAGGGAAAGTGATTCTTATGAGAAGCAATGTTTTGGATTTCACTGAATTTCAT 227 Qy Db 241 AGTGCCACTCATACTTCAAATGACTCAAGAGGGAAAGTTGGGAACAAGGCATATTTGGAG 300 Qy Db 288 AGTGCCACTCATACTTCAAATGACTCAAGAGGGAAAGTTGGGAACAAGGCATATTTGGAG 347 301 AGGTGGCTAACTTCAATCCCACCACTGTTTGCTGGAGAATCAGTGTTCCAAATCAACTTT 360 Qy Db 348 AGGTGGCTAACTTCAATCCCACCACTGTTTGCTGGAGAATCAGTGTTCCAAATCAACTTT 407 361 CAATGGGATGAAAATTTTGGATTTCCAGGAGCTTTCTTCATAAAAAATGGACATACAAGT 420 Qу 408 CAATGGGATGAAAATTTTGGATTTCCAGGAGCTTTCTTCATAAAAAATGGACATACAAGT 467 Db 421 GAATTCTTTCTCAAATCTCTCACTCTTGATGATGTTCCTGGCTATGGCAGAGTCCATTTT 480 QУ 468 GAATTCTTTCTCAAATCTCTCACTCTTGATGATGTTCCTGGCTATGGCAGAGTCCATTTT 527 Db 481 GATTGCAATTCTTGGGTTTACCCTTCTGGAAGATACAAGAAGATCGCATTTTCTTTGCC 540 Qу Db 541 AATCATGTTTATCTTCCAAGTCAAACACCAAACCCTCTTCGTAAGTATAGAGAGGAAGAA 600 Qy 588 AATCATGTTTATCTTCCAAGTCAAACACCAAACCCTCTTCGTAAGTATAGAGAGGAAGAA 647 Db 601 TTGTGGAATTTGAGAGGAGATGGAACAGGAGAAAGAAAGGAATGGGATAGAATTTATGAC 660 Qу Db 648 TTGTGGAATTTGAGAGGAGATGGAACAGGAGAAGGAATGGGATAGAATTTATGAC 707 Qу 661 TATGATGTTTATAATGACATTGCTGACCCTGATGTTGGTGATCATCGTCCTATTCTCGGT 720 708 TATGATGTTTATAATGACATTGCTGACCCTGATGTTGGTGATCATCGTCCTATTCTCGGT 767 Db 721 GGGACGACCGAA 732 Qy ! | | ! | | | | | | | | Db 768 GGGACGACCGAA 779

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RESULT 2
CSLBLOX
LOCUS
                                                mRNA
                                                        linear
                                                                 PLN 18-MAR-2001
            CSLBLOX
                                     2964 bp
DEFINITION C.sativus mRNA for lipoxygenase.
ACCESSION
            X92890.1 GI:1296511
VERSION
KEYWORDS
            lipoxygenase.
SOURCE
            Cucumis sativus (cucumber)
  ORGANISM Cucumis sativus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
REFERENCE
  AUTHORS
            Hohne, M., Nellen, A., Schwennesen, K. and Kindl, H.
  TITLE
            Lipid body lipoxygenase characterized by protein fragmentation,
            cDNA sequence and very early expression of the enzyme during
            germination of cucumber seeds
  JOURNAL
            Eur. J. Biochem. 241 (1), 6-11 (1996)
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            8898881
REFERENCE
            2 (bases 1 to 2964)
  AUTHORS
            Kindl, H.
  TITLE
            Direct Submission
  JOURNAL
            Submitted (10-NOV-1995) H. Kindl, FB Chemie, Universitat Marburg,
            Hans-Meerwein-Strasse, D- Marburg, FRG
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                     /db_xref="SPTREMBL:Q42710"
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                     DCNSWVYPSGRYKKDRIFFANHVYLPSQTPNPLRKYREEELWNLRGDGTGERKEWDRI
                     YDYDVYNDIADPDVGDHRPILGGTTEYPYPRRGRTGRPRSRRDHNYESRLSPIMSLDI
                     YVPKDENFGHLKMSDFLGYTLKALSISIKPGLQSIFDVTPNEFDNFKEVDNLFERGFP
                     IPFNAFKTLTEDLTPPLFKALVRNDGEKFLKFPTPEVVKDNKIGWSTDEEFAREMLAG
                     PNPLLIRRLEAFPPTSKLDPNVYGNQNSTITEEHIKHGLDGLTVDEAMKQNRLYIVDF
                     HDALMPYLTRMNATSTKTYATRTLLLLKDDGTLKPLVIELALPHPQGDQLGAISKLYF
                     PAENGVQKSIWQLAKAYVTVNDVGYHQLISHWLHTHAVLEPFVIATHRQLSVLHPIHK
                     LLVPHYKDTMFINASARQVLINANGLIETTHYPSKYSMELSSILYKDWTFPDQALPNN
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                     TLLVPSSNEGLTGRGIPNSISI"
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100.0%; Query Match Score 2964; DB 8; Length 2964; Best Local Similarity 100.0%; Pred. No. 0; Matches 2964; Conservative Mismatches 0; Indels Gaps 0; 1 GTTCCAAACACACAGTGAGCAAAAAAGAAAAGTAAAAAAGAGTGAAAATGTTTGGAATTG 60 Qу Db 1 GTTCCAAACACACGTGAGCAAAAAGAAAAGTAAAAAAGAGTGAAAATGTTTGGAATTG 60 61 GGAAGAACATCATTGAAGGGGCCTTGAATACAACTGGAGATCTTGCAGGTTCTGTTATCA 120 Qу 61 GGAAGAACATCATTGAAGGGGCCTTGAATACAACTGGAGATCTTGCAGGTTCTGTTATCA 120 Db 121 ATGCTGGTGGTAACATTTTAGATAGAGTTTCCAGTCTTGGAGGAAACAAAATCAAAGGGA 180 Qу 121 ATGCTGGTGGTAACATTTTAGATAGAGTTTCCAGTCTTGGAGGAAACAAAATCAAAGGGA 180 Db 181 AAGTGATTCTTATGAGAAGCAATGTTTTGGATTTCACTGAATTTCATTCCAATCTTCTTG 240 Qу Db 181 AAGTGATTCTTATGAGAAGCAATGTTTTGGATTTCACTGAATTTCATTCCAATCTTCTTG 240 241 ATAACTTCACTGAGCTCTTGGGTGGTGTTTCTTTCCAACTCATTAGTGCCACTCATA 300 Qy Db 241 ATAACTTCACTGAGCTCTTGGGTGGTGTTTCTTTCCAACTCATTAGTGCCACTCATA 300 301 CTTCAAATGACTCAAGAGGGAAAGTTGGGAACAAGGCATATTTGGAGAGGTGGCTAACTT 360 Qу Db 301 CTTCAAATGACTCAAGAGGGAAAGTTGGGAACAAGGCATATTTGGAGAGGTGGCTAACTT 360 361 CAATCCCACCACTGTTTGCTGGAGAATCAGTGTTCCAAATCAACTTTCAATGGGATGAAA 420 Qу 361 CAATCCCACCACTGTTTGCTGGAGAATCAGTGTTCCAAATCAACTTTCAATGGGATGAAA 420 Db Qу Db Qу 481 AATCTCTCACTCTTGATGATGTTCCTGGCTATGGCAGAGTCCATTTTGATTGCAATTCTT 540 481 AATCTCTCACTCTTGATGATGTTCCTGGCTATGGCAGAGTCCATTTTGATTGCAATTCTT 540 Db 541 GGGTTTACCCTTCTGGAAGATACAAGAAGATCGCATTTTCTTTGCCAATCATGTTTATC 600 Qу Db 541 GGGTTTACCCTTCTGGAAGATACAAGAAAGATCGCATTTTCTTTGCCAATCATGTTTATC 600 601 TTCCAAGTCAAACACCAAACCCTCTTCGTAAGTATAGAGAGGAAGAATTGTGGAATTTGA 660 Qу 601 TTCCAAGTCAAACACCAAACCCTCTTCGTAAGTATAGAGAGGAAGAATTGTGGAATTTGA 660 Db 661 GAGGAGATGGAACAGGAAAGGAAAGGAATGGGATAGAATTTATGACTATGATGTTTATA 720 Qу 661 GAGGAGATGGAACAGGAAAGAAAGGAATGGGATAGAATTTATGACTATGATGTTTATA 720 Db 721 ATGACATTGCTGACCCTGATGTTGGTGATCATCGTCCTATTCTCGGTGGGACGACCGAAT 780 Qу Db 721 ATGACATTGCTGACCCTGATGTTGGTGATCATCGTCCTATTCTCGGTGGGACGACCGAAT 780

Qy	781	ATCCTTACCCTCGTAGGGGAAGAACAGGACGACCACGATCAAGAAGAGACCACAATTATG	840
Db	781		840
Qy	841	AGAGCAGATTGTCACCAATAATGAGCTTAGACATCTATGTACCAAAAGATGAAAACTTTG	900
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Qy	901	GGCATTTGAAGATGTCAGATTTCCTTGGTTATACATTAAAAGCACTTTCGATATCAATCA	960
Db	901	GGCATTTGAAGATGTCAGATTTCCTTGGTTATACATTAAAAGCACTTTCGATATCAATCA	960
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Db	961	AACCAGGACTTCAATCCATATTTGATGTAACTCCAAATGAATTTGACAATTTTAAAGAAG	1020
Qy	1021	TTGATAATCTCTTTGAGAGAGGTTTTCCCATTCCATTTAATGCTTTTAAGACCCTCACTG	1080
Db	1021	TTGATAATCTCTTTGAGAGAGGTTTTCCCATTCCATTTAATGCTTTTAAGACCCTCACTG	1080
Qy	1081	AGGACCTCACCTCTGTTCAAAGCACTCGTGAGGAATGATGGTGAAAAATTCCTCA	1140
Db	1081	AGGACCTCACCTCTGTTCAAAGCACTCGTGAGGAATGATGGTGAAAAATTCCTCA	1140
Qy	1141	AATTTCCTACTCCCGAAGTTGTCAAAGATAATAAAATAGGATGGAGCACTGATGAAGAAT	1200
Db	1141		1200
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Db	1621	ATGTAACTGTTAATGATGTTGGCTACCATCAACTTATTAGTCATTGGTTGCATACTCATG	1680
Qy	1681	CTGTACTTGAGCCATTTGTGATTGCAACACATAGACAATTGAGCGTGCTTCATCCAATCC	1740
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Qу	1921	TCATGAAGAGAGGACTAGCTGTGGAGGACTCAAGTGCCCCCCATGGACTTAGATTGCTAA	1980
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Qу	2341	AACTGGAATCGAATCCCGAAAAAGCTTTCTTGAGAACAATATGTTCAGAATTACAAGCAC	2400
Db	2341	AACTGGAATCGAATCCCGAAAAAGCTTTCTTGAGAACAATATGTTCAGAATTACAAGCAC	2400
Qy	2401	TTGTTAGTATTTCAATTATTGAAATCTTGTCAAAGCATGCTTCTGATGAAGTTTATCTTG	2460
Db	2401	TTGTTAGTATTTCAATTATTGAAATCTTGTCAAAGCATGCTTCTGATGAAGTTTATCTTG	2460
QУ	2461	GACAAAGAGCTTCAATTGATTGGACTTCAGATAAAATTGCATTGGAAGCATTTGAGAAAT	2520

Db	2461	${\tt GACAAAGAGCTTCAATTGATTGGACTTCAGATAAAATTGCATTGGAAGCATTTGAGAAAT}$	2520
Qy	2521	TTGGGAAAAATTTATTTGAAGTTGAGAATAGGATCATGGAAAGGAATAAAGAGGTGAATT	2580
Db	2521	TTGGGAAAAATTTATTTGAAGTTGAGAATAGGATCATGGAAAGGAATAAAGAGGTGAATT	2580
Qy	2581	TGAAGAATAGATCTGGACCTGTTAATTTGCCTTATACTCTACTTGTTCCATCAAGTAACG	2640
Db	2581	TGAAGAATAGATCTGGACCTGTTAATTTGCCTTATACTCTACTTGTTCCATCAAGTAACG	2640
Qy	2641	AAGGACTCACTGGAAGAGGAATTCCTAATAGTATTTCTATCTA	2700
Db	2641	AAGGACTCACTGGAAGAGGAATTCCTAATAGTATTTCTATCTA	2700
Qy	2701	AGTGGTTCTTTTATGGGTGACGTGTGTAATTTGAAGGTCACAAATTACATTTTAAGTTG	2760
Db	2701	AGTGGTTCTTTTATGGGTGACGTGTAATTTGAAGGTCACAAATTACATTTTAAGTTG	2760
Qy	2761	CCCACATTATTATGAAGGAAATAAATGACCATATTTTTAGTTTAATTTAAATTAGGT	2820
Db .	2761	CCCACATTATTATGAAGGAAATAAATGACCATATTTTTAGTTTAATTTAAATTAGGT	2820
Qу	2821	AGCTATAGCCAACTTTAGGCTCTGTTGGATTTGGAACTATCTCCAACTTATATATGTACT	2880
Db	2821	AGCTATAGCCAACTTTAGGCTCTGTTGGATTTGGAACTATCTCCAACTTATATATGTACT	2880
Qy	2881	TTGTACTACTATTGATGAATAAAAGTTGTGTGTCTTAAGAATAAAAAAAA	2940
Db	2881	TTGTACTACTATTTGATGAATAAAAGTTGTGTGTCTTAAGAATAAAAAAAA	2940
Qу	2941	AAAAAAAAAAAAAAAAAAA 2964 	
Db	2941		

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tr anales Aktenzeichen
PCT/EP 00/09912

A. KLASSI IPK 7	FIZIERUNG DES ANMELDUNGSGEGENSTANDES C12N15/53 C12N9/02 A01H5/00	C12N5/10	A01K67/00				
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	RCHIERTE GEBIETE						
Recherchierter Mindestprüfstoff (Klassifikationssystem und Klassifikationssymbole) IPK 7 C12N A01K A01H							
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Während de	er internationalen Recherche konsultierte elektronische Datenbank (N	lame der Datenbank und evtl. v	erwendete Suchbegriffe)				
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A	TATULIAN SUREN A: "Ca2+-depender membrane binding of soybean lipoxygenase-1: Possible implicat the N-terminal beta-barrel domain FASEB JOURNAL, Bd. 12, Nr. 8, 24. April 1998 (1998-04-24), Seit XP000982453 Meeting of the American Society f Biochemistry and Molecular Biology; Washington, D.C., USA; Ma1998 ISSN: 0892-6638 DE 196 41 158 A (SCHMIDT M A) 9. April 1998 (1998-04-09)	tion of 1." te A1285					
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	3. Februar 2001	06/03/2001					
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